

MDQSSRRDES YHETHPGSLDP SHQSHPHPHPTLHRPNQGGVYYDSPQH 50
GMFQQPYQQHGGFHQQNELQHLREFSDSHDNAFSHHSYQQDRAGVSTLPN 100
NISHAYGSGHP LAESQHSGGPQSGPRIDPNHHPHQDDPHRPSEPLSHPSS 150
TGSHQGTTHQQYHERSHHLNPQQNRDHADTISYRSSTRFYRSHAPFSRQE 200
RPHLHADHHHEGHHASHHGEHPHKEQRHYHGDHMHMHHIHHRSPSASQL 250
SEGEDHVQKRKKAQRAHKKAHGTGNIFQLLWEKISHLLGLQQMILSLTQS 350

S1

LGFETFI FIVVCLNTVILVAQT FTELEIRGEWYF MVLD SIFLSIYVLEAV 400

S2

LKLI ALGLE YFYDPWNNLD FFI MVMAVLD FVLLQ INSL SYSFYNHSL FRI 450

S4

LKVF KSMRALRAIRVLRRLS ILTSLHEVAGT LSGSLPS I TAIL TLMFTCL 500

S5

FLFSVVLRAL FQDSDPKRFRQN IFTT LFTLFTMLTLDDWSLI YIDNRAQGA 550

S6

WYIIPILMIYI VIQYFI FLNLVIAVL VDNFQMA LLKGLEKVKLEQAARVH 600
EKLDDSLTDLNKADANAQMT EALKMQLIEGMFGNMTVKQRVLHFQFLQ 650
LVAAVEHQQKFRSQAYVIDELVDMAFEAGDDDYCK 686

P

FIG. 1A

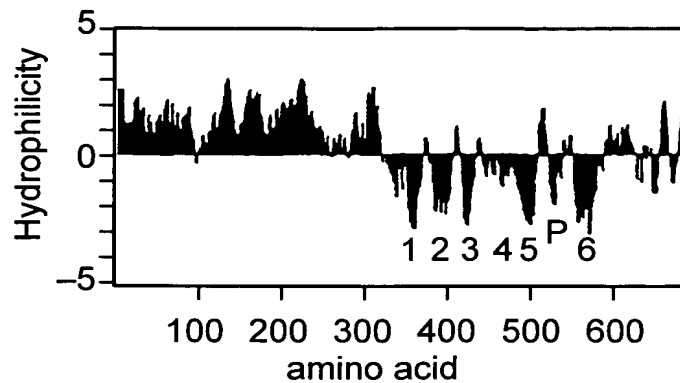


FIG. 1B

Pore region	
CatSper	RFQNI FTTLFTLFTMLTLD DWSLIYID
I Cav1.2	NFDNFAFAMLTVFQCI TMEGWTDVLYN
I Cav2.2	NFDNILFAILTVFQCI TMEGWTDILYN
Cav3.1	NFDNIGYAWIAIFQVITLEGWVDIMYF
II Cav1.2	TFDNFPQSLLTVFQILTGEDWNSVMYD
II Cav2.2	NFDTFPAAILTVFQILTGEDWNAVMYN
Cav3.1	NFDSLLWAIVTVFQILTQEDWNKVLYN
III Cav1.2	DFDNVLAAMMALFTVSTFEGWPPELLYR
III Cav2.2	HYDNVLWALLTLFTVSTGEGWPMYLKH
Cav3.1	NFDNLGQALMSLFVLASKDGVVDIMYD
IV Cav1.2	NFQTFPQAVLLLP RCATGEAWQDIMLA
IV Cav2.2	NFRTFLQALMLLFRSATGEAWHEIMLS
Cav3.1	TFRNFGMAFLTFRVSTGDNWNGIMKD

FIG. 1C

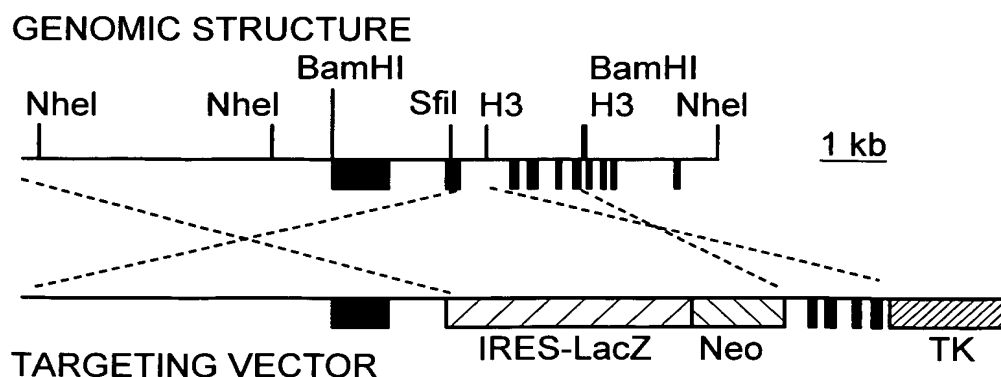


FIG. 2

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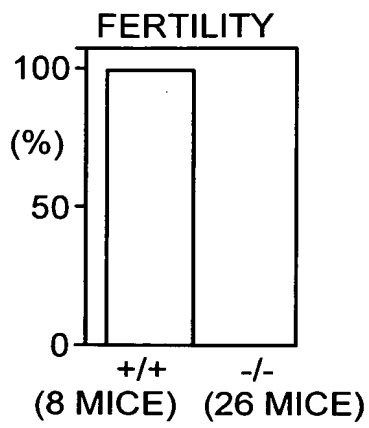


FIG. 3A

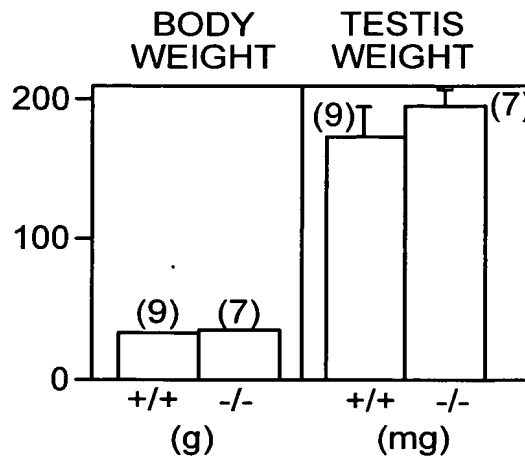


FIG. 3B

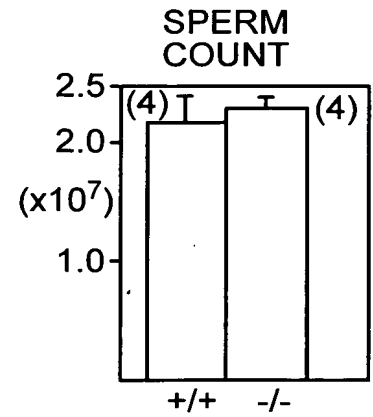


FIG. 3C

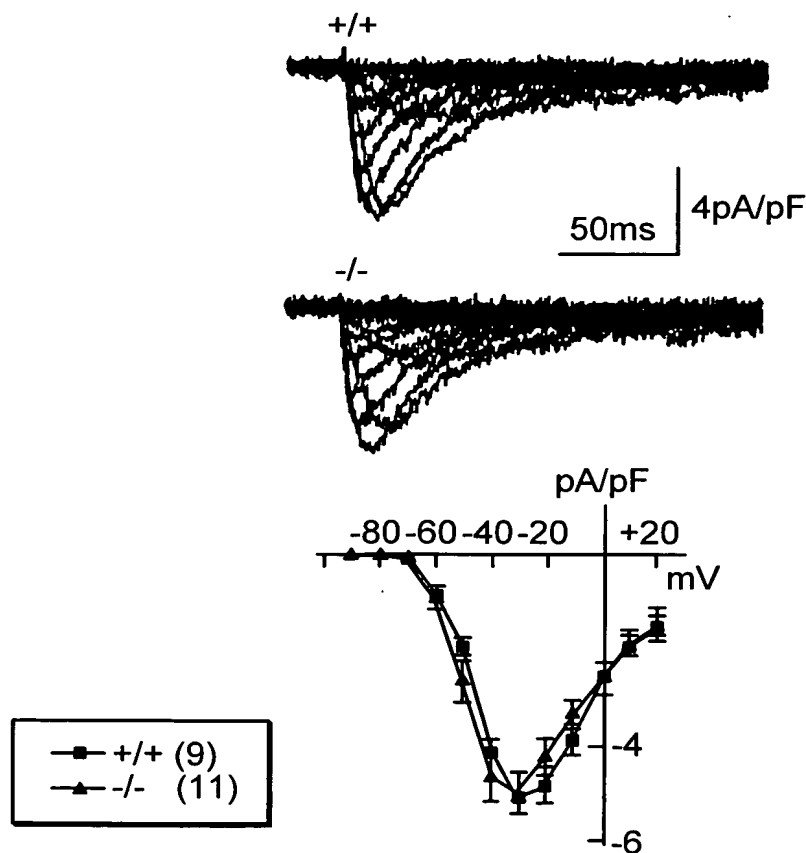


FIG. 3D

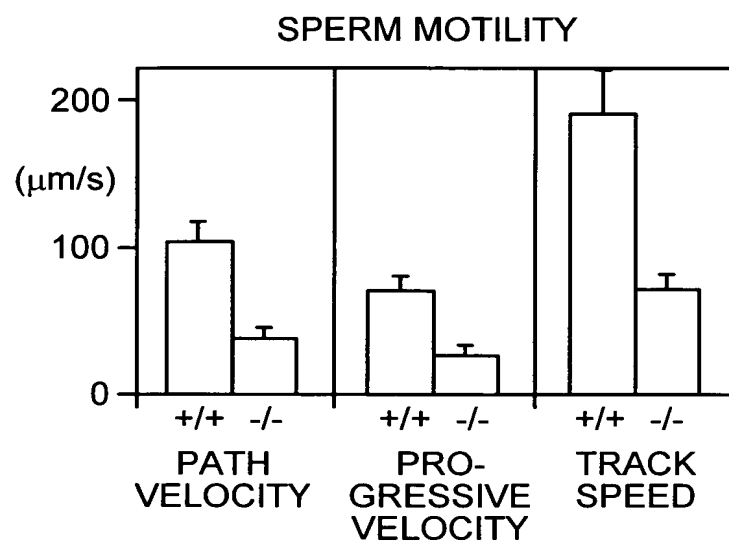


FIG. 4A

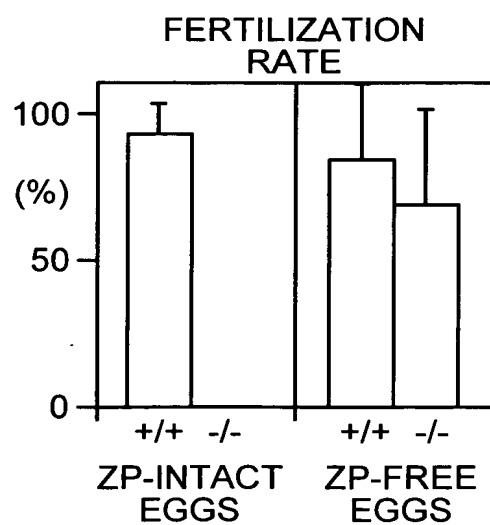


FIG. 4B

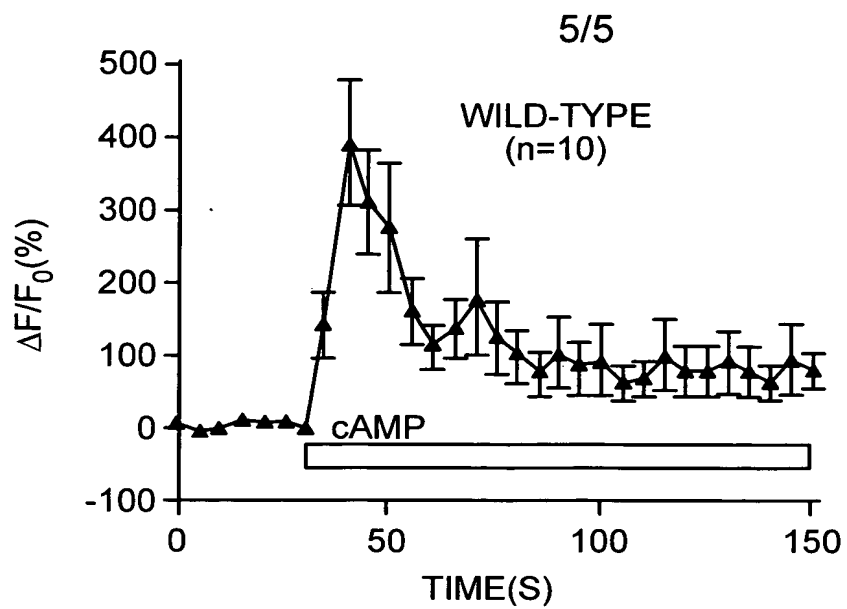


FIG. 5A-1

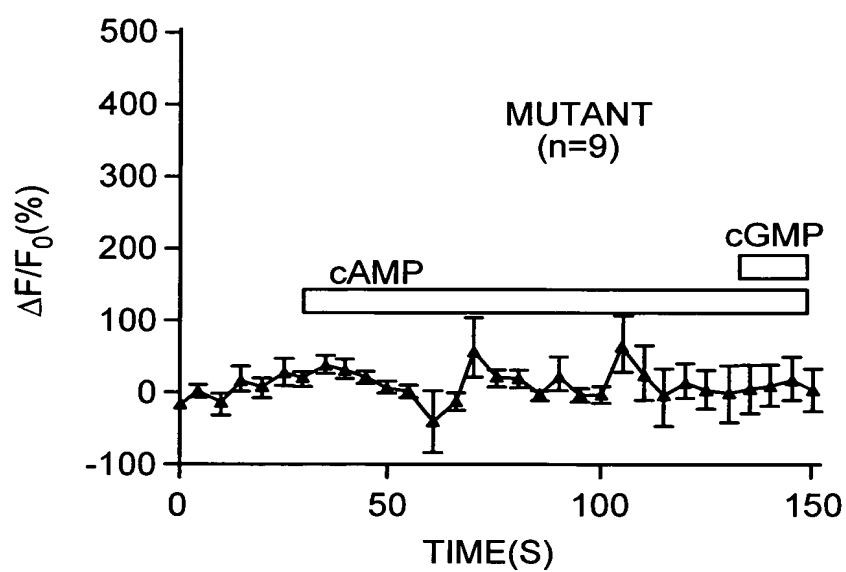


FIG. 5A-2

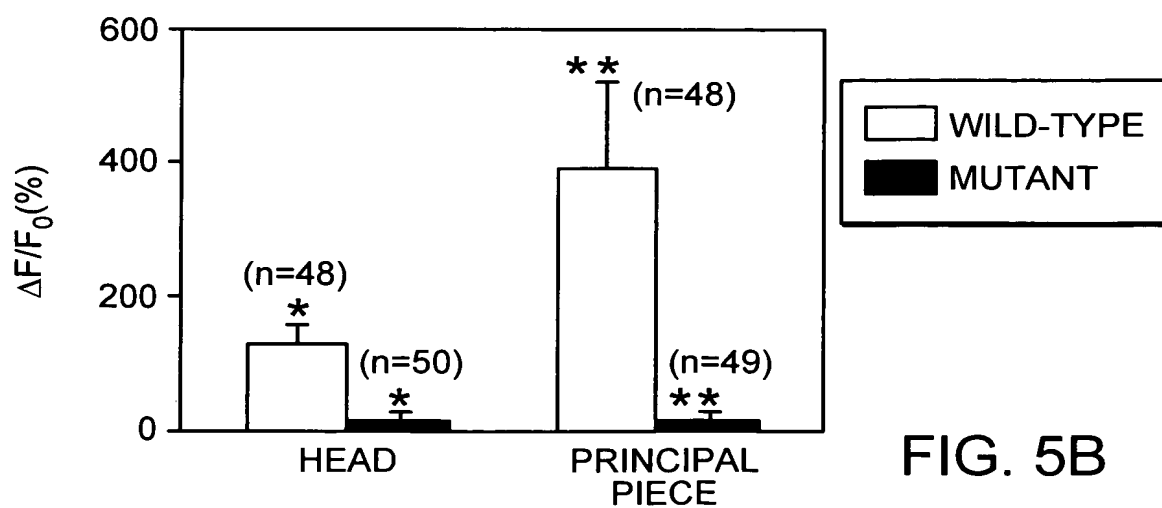


FIG. 5B